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#3

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# SEQUENCE LISTING

<110> Kovesdi, Imre  
Kessler, Paul

<120> VEGF FUSION PROTEINS

<130> 205654

<140> US 09/832,355

<141> 2001-04-10

<160> 126

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35 40 45

Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu  
50 55 60

Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile  
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Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe  
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           50                          55                          60  
 Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln Gly  
           65                          70                          75                          80  
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Ala Arg Gln Glu Lys Cys  
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Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro  
 35 40 45

Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr  
 50 55 60

Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser  
 65 70 75 80

Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp  
 85 90 95

Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met  
 100 105 110

Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu  
 115 120 125

Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys  
 130 135 140

Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu  
 145 150 155 160

Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln  
 165 170 175

Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser  
 180 185 190

Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu  
 195 200 205

Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr  
 210 215 220

Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala  
 225 230 235 240

Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp  
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 Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu  
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 Lys Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp  
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 Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn  
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 Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp  
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 Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn  
 385 390 395 400  
 Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser  
 405 410 415  
 Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn  
 420 425 430  
 Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp  
 435 440 445  
 Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala  
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&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

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Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln
20          25          30

Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu
35          40          45

Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln
50          55          60

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Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr  
65 70 75 80

Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg  
85 90 95

Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu  
100 105 110

Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn  
115 120 125

Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp  
130 135 140

Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln  
145 150 155 160

Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro  
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Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe  
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35 40 45

Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met Ala  
50 55 60

Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu Glu  
65 70 75 80

Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys Leu  
85 90 95

Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu Ile  
100 105 110

Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln Leu  
115 120 125

Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser Leu  
130 135 140

Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu Leu

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 Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr Arg  
                                  165                      170                      175  
 Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala Thr  
                                  180                      185                      190  
 Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp Thr  
                                  195                      200                      205  
 Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu Lys  
                                  210                      215                      220  
 Gly Gly Lys Arg Glu Glu Glu Lys Pro Phe Arg  
 225                      230                      235

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                                  20                      25                      30  
 Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro  
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Glu

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His Arg Leu Pro Arg Asp Cys Gln Glu Leu Phe Gln Val Gly Glu Arg  
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 Gln Ser Gly Leu Phe Glu Ile Gln Pro Gln Gly Ser Pro Pro Phe Leu  
                                  20                      25                      30  
 Val Asn Cys Lys Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg  
                                  35                      40                      45  
 Arg His Asp Gly Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys  
                                  50                      55                      60  
 Ala Gly Phe Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys  
 65                      70                      75                      80  
 Val His Ser Ile Met Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu  
                                  85                      90                      95

Arg Asp Trp Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu  
                   100                  105                  110

Gly Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala  
                   115                  120                  125

Gly Gln Leu Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro  
                   130                  135                  140

Phe Ser Thr Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys  
 145                  150                  155                  160

Ala Lys Ser Leu Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser  
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Asn Leu Asn Gly Gln Tyr Phe Arg  
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Glu Glu Gln Ile Ser Phe Arg Asp Cys Ala Glu Val Phe Lys Ser Gly  
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His Thr Thr Asn Gly Ile Tyr Thr Leu Thr Phe Pro Asn Ser Thr Glu  
                   20                  25                  30

Glu Ile Lys Ala Tyr Cys Asp Met Glu Ala Gly Gly Gly Gly Trp Thr  
                   35                  40                  45

Ile Ile Gln Arg Arg Glu Asp Gly Ser Val Asp Phe Gln Arg Thr Trp  
                   50                  55                  60

Lys Glu Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu  
 65                  70                  75                  80

Gly Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg Tyr Val Leu  
                   85                  90                  95

Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr Ser Leu Tyr  
                   100                  105                  110

Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg Ile His Leu  
                   115                  120                  125

Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile Ser Gln Pro  
                   130                  135                  140

Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys Cys Ile Cys  
 145                  150                  155                  160

Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly  
                   165                  170                  175

Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln Asn Thr Asn  
 180 185 190

Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser Gly Tyr Ser  
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Leu Lys Ala Thr Thr Met Met Ile Arg Pro Ala Asp Phe  
 210 215 220

<210> 22

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<213> Homo sapiens

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Lys Met Gly Pro Lys Gly Glu Pro Gly Pro Arg Asn Cys Arg Glu Leu  
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Leu Ser Gln Gly Ala Thr Leu Ser Gly Trp Tyr His Leu Cys Leu Pro  
 20 25 30

Glu Gly Arg Ala Leu Pro Val Phe Cys Asp Met Asp Thr Glu Gly Gly  
 35 40 45

Gly Trp Leu Val Phe Gln Arg Arg Gln Asp Gly Ser Val Asp Phe Phe  
 50 55 60

Arg Ser Trp Ser Ser Tyr Arg Ala Gly Phe Gly Asn Gln Glu Ser Glu  
 65 70 75 80

Phe Trp Leu Gly Asn Glu Asn Leu His Gln Leu Thr Leu Gln Gly Asn  
 85 90 95

Trp Glu Leu Arg Val Glu Leu Glu Asp Phe Asn Gly Asn Arg Thr Phe  
 100 105 110

Ala His Tyr Ala Thr Phe Arg Leu Leu Gly Glu Val Asp His Tyr Gln  
 115 120 125

Leu Ala Leu Gly Lys Phe Ser Glu Gly Thr Ala Gly Asp Ser Leu Ser  
 130 135 140

Leu His Ser Gly Arg Pro Phe Thr Thr Tyr Asp Ala Asp His Asp Ser  
 145 150 155 160

Ser Asn Ser Asn Cys Ala Val Ile Val His Gly Ala Trp Trp Tyr Ala  
 165 170 175

Ser Cys Tyr Arg Ser Asn Leu Asn Gly Arg Tyr Ala Val Ser Glu Ala  
 180 185 190

Ala Ala His Lys Tyr Gly Ile Asp Trp Ala Ser Gly Arg Gly Val Gly  
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His Pro Tyr Arg Arg Val Arg Met Met Leu Arg  
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          20          25          30

Cys Asp Met Glu Thr Ser Gly Gly Gly Trp Thr Ile Ile Gln Arg Arg
          35          40          45

Lys Ser Gly Leu Val Ser Phe Tyr Arg Asp Trp Lys Gln Tyr Lys Gln
          50          55          60

Gly Phe Gly Ser Ile Arg Gly Asp Phe Trp Leu Gly Asn Glu His Ile
65          70          75          80

His Arg Leu Ser Arg Gln Pro Thr Arg Leu Arg Val Glu Met Glu Asp
          85          90          95

Trp Glu Gly Asn Leu Arg Tyr Ala Glu Tyr Ser His Phe Val Leu Gly
          100          105          110

Asn Glu Leu Asn Ser Tyr Arg Leu Phe Leu Gly Asn Tyr Thr Gly Asn
          115          120          125

Val Gly Asn Asp Ala Leu Gln Tyr His Asn Asn Thr Ala Phe Ser Thr
          130          135          140

Lys Asp Lys Asp Asn Asp Asn Cys Leu Asp Lys Cys Ala Gln Leu Arg
145          150          155          160

Lys Gly Gly Tyr Trp Tyr Asn Cys Cys Thr Asp Ser Asn Leu Asn Gly
          165          170          175

Val Tyr Tyr Arg Leu Gly Glu His Asn Lys His Leu Asp Gly Ile Thr
          180          185          190

Trp Tyr Gly Trp His Gly Ser Thr Tyr Ser Leu Lys Arg Val Glu Met
          195          200          205

Lys Ile Arg Pro Glu Asp Phe Lys Pro
          210          215

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1          5          10          15

His Glu Gln Ser Gly Val Tyr Glu Leu Arg Val Gly Arg His Val Val

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15.

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<210> 25
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1				5					10					15	
Gly	Leu	Phe	Glu	Ile	Gln	Pro	Gln	Gly	Ser	Pro	Pro	Phe	Leu	Val	Asn
			20					25					30		
Cys	Lys	Met	Thr	Ser	Asp	Gly	Gly	Trp	Thr	Val	Ile	Gln	Arg	Arg	His
		35					40					45			
Asp	Gly	Ser	Val	Asp	Phe	Asn	Arg	Pro	Trp	Glu	Ala	Tyr	Lys	Ala	Gly
	50					55					60				
Phe	Gly	Asp	Pro	His	Gly	Glu	Phe	Trp	Leu	Gly	Leu	Glu	Lys	Val	His
65					70					75					80



Ser Ile Thr Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg Asp  
85 90 95

Trp Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly Gly  
100 105 110

Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln  
115 120 125

Leu Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser  
130 135 140

Thr Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys  
145 150 155 160

Ser Leu Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu  
165 170 175

Asn Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys  
180 185 190

Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu Gln  
195 200 205

Ala Thr Thr Met Leu Ile Gln  
210 215

<210> 26  
<211> 222  
<212> PRT  
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<220>  
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<223> Source not known

<400> 26

Pro Arg Asp Cys Gln Glu Leu Phe Gln Val Gly Glu Arg Gln Ser Gly  
1 5 10 15

Leu Phe Glu Ile Gln Pro Gln Gly Ser Pro Pro Phe Leu Val Asn Cys  
20 25 30

Lys Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg His Asp  
35 40 45

Gly Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala Gly Phe  
50 55 60

Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val His Ser  
65 70 75 80

Ile Thr Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg Asp Trp  
85 90 95

Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly Gly Glu

100	105	110
Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln Leu		
115	120	125
Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser Thr		
130	135	140
Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys Ser		
145	150	155
Leu Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn		
165	170	175
Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys Lys		
180	185	190
Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu Gln Ala		
195	200	205
Thr Thr Met Leu Ile Gln Pro Met Ala Ala Glu Ala Ala Ser		
210	215	220

<210> 27  
 <211> 222  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Source not known

<400> 27

His Asp Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu	
1 5 10 15	
His Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe	
20 25 30	
His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln	
35 40 45	
His Arg Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr	
50 55 60	
Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu	
65 70 75 80	
Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu	
85 90 95	
Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr	
100 105 110	
Leu Gly Asn His Glu Thr Asn Tyr Thr Leu His Leu Val Ala Ile Thr	
115 120 125	

Gly Asn Val Pro Asn Ala Ile Pro Glu Asn Lys Asp Leu Val Phe Ser  
 130 135 140

Thr Trp Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr  
 145 150 155 160

Ser Gly Gly Trp Trp Trp His Asp Glu Cys Gly Glu Asn Asn Leu Asn  
 165 170 175

Gly Lys Tyr Asn Lys Pro Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg  
 180 185 190

Gly Leu Ser Trp Lys Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser  
 195 200 205

Thr Lys Met Leu Ile His Pro Thr Asp Ser Glu Ser Phe Glu  
 210 215 220

<210> 28

<211> 214

<212> PRT

<213> Mus musculus

<400> 28

Arg Asp Cys Gln Glu Leu Phe Gln Glu Gly Glu Arg His Ser Gly Leu  
 1 5 10 15

Phe Gln Ile Gln Pro Leu Gly Ser Pro Pro Phe Leu Val Asn Cys Glu  
 20 25 30

Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg Leu Asn Gly  
 35 40 45

Ser Val Asp Phe Asn Gln Ser Trp Glu Ala Tyr Lys Asp Gly Phe Gly  
 50 55 60

Asp Pro Gln Gly Glu Phe Trp Leu Gly Leu Glu Lys Met His Ser Ile  
 65 70 75 80

Thr Gly Asn Arg Gly Ser Gln Leu Ala Val Gln Leu Gln Asp Trp Asp  
 85 90 95

Gly Asn Ala Lys Leu Leu Gln Phe Pro Ile His Leu Gly Gly Glu Asp  
 100 105 110

Thr Ala Tyr Ser Leu Gln Leu Thr Glu Pro Thr Ala Asn Glu Leu Gly  
 115 120 125

Ala Thr Asn Val Ser Pro Asn Gly Leu Ser Leu Pro Phe Ser Thr Trp  
 130 135 140

Asp Gln Asp His Asp Leu Arg Gly Asp Leu Asn Cys Ala Lys Ser Leu  
 145 150 155 160

Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn Gly  
 165 170 175

Gln Tyr Phe His Ser Ile Pro Arg Gln Arg Gln Glu Arg Lys Lys Gly

180 185 190  
 Ile Phe Trp Lys Thr Trp Lys Gly Arg Tyr Tyr Pro Leu Gln Ala Thr  
 195 200 205  
 Thr Leu Leu Ile Gln Pro  
 210  
 <210> 29  
 <211> 216  
 <212> PRT  
 <213> Homo sapiens  
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 Phe Gln Asp Cys Ala Glu Ile Lys Arg Ser Gly Val Asn Thr Ser Gly  
 1 5 10 15  
 Val Tyr Thr Ile Tyr Glu Thr Asn Met Thr Lys Pro Leu Lys Val Phe  
 20 25 30  
 Cys Asp Met Glu Thr Asp Gly Gly Gly Trp Thr Leu Ile Gln His Arg  
 35 40 45  
 Glu Asp Gly Ser Val Asn Phe Gln Arg Thr Trp Glu Glu Tyr Lys Glu  
 50 55 60  
 Gly Phe Gly Asn Val Ala Arg Glu His Trp Leu Gly Asn Glu Ala Val  
 65 70 75 80  
 His Arg Leu Thr Ser Arg Thr Ala Tyr Leu Leu Arg Val Glu Leu His  
 85 90 95  
 Asp Trp Glu Gly Arg Gln Thr Ser Ile Gln Tyr Glu Asn Phe Gln Leu  
 100 105 110  
 Gly Ser Glu Arg Gln Arg Tyr Ser Leu Ser Val Asn Asp Ser Ser Ser  
 115 120 125  
 Ser Ala Gly Arg Lys Asn Ser Leu Ala Pro Gln Gly Thr Lys Phe Ser  
 130 135 140  
 Thr Lys Asp Met Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Gln Met  
 145 150 155 160  
 Leu Ser Gly Gly Trp Trp Phe Asp Ala Cys Gly Leu Ser Asn Leu Asn  
 165 170 175  
 Gly Ile Tyr Tyr Ser Val His Gln His Leu His Lys Ile Asn Gly Ile  
 180 185 190  
 Arg Trp His Tyr Phe Arg Gly Pro Ser Tyr Ser Leu His Gly Thr Arg  
 195 200 205  
 Met Met Leu Arg Pro Met Gly Ala  
 210 215  
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LVM 205654

20

<212> PRT

<213> Homo sapiens

<400> 30

Phe Gln Asp Cys Ala Glu Ile Gln Arg Ser Gly Ala Ser Ala Ser Gly  
1 5 10 15

Val Tyr Thr Ile Gln Val Ser Asn Ala Thr Lys Pro Arg Lys Val Phe  
20 25 30

Cys Asp Leu Gln Ser Ser Gly Gly Arg Trp Thr Leu Ile Gln Arg Arg  
35 40 45

Glu Asn Gly Thr Val Asn Phe Gln Arg Asn Trp Lys Asp Tyr Lys Gln  
50 55 60

Gly Phe Gly Asp Pro Ala Gly Glu His Trp Leu Gly Asn Glu Val Val  
65 70 75 80

His Gln Leu Thr Arg Arg Ala Ala Tyr Ser Leu Arg Val Glu Leu Gln  
85 90 95

Asp Trp Glu Gly His Glu Ala Tyr Ala Gln Tyr Glu His Phe His Leu  
100 105 110

Gly Ser Glu Asn Gln Leu Tyr Arg Leu Ser Val Val Gly Tyr Ser Gly  
115 120 125

Ser Ala Gly Arg Gln Ser Ser Leu Val Leu Gln Asn Thr Ser Phe Ser  
130 135 140

Thr Leu Asp Ser Asp Asn Asp His Cys Leu Cys Lys Cys Ala Gln Val  
145 150 155 160

Met Ser Gly Gly Trp Trp Phe Asp Ala Cys Gly Leu Ser Asn Leu Asn  
165 170 175

Gly Val Tyr Tyr His Ala Pro Asp Asn Lys Tyr Lys Met Asp Gly Ile  
180 185 190

Arg Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ala Ser Arg  
195 200 205

Met Met Ile Arg Pro Leu Asp Ile  
210 215

<210> 31

<211> 224

<212> PRT

<213> Homo sapiens

<400> 31

Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly  
1 5 10 15

His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn Arg  
20 25 30

<400> 32

Ile	Asn	Glu	Gly	Pro	Phe	Lys	Asp	Cys	Gln	Gln	Ala	Lys	Glu	Ala	Gly
1				5					10					15	
His	Ser	Val	Ser	Gly	Ile	Tyr	Met	Ile	Lys	Pro	Glu	Asn	Ser	Asn	Gly
			20					25					30		
Pro	Met	Gln	Leu	Trp	Cys	Glu	Asn	Ser	Leu	Asp	Pro	Gly	Gly	Trp	Thr
		35					40					45			
Val	Ile	Gln	Lys	Arg	Thr	Asp	Gly	Ser	Val	Asn	Phe	Phe	Arg	Asn	Trp
	50					55					60				
Glu	Asn	Tyr	Lys	Lys	Gly	Phe	Gly	Asn	Ile	Asp	Gly	Glu	Tyr	Trp	Leu
65					70					75					80

22

Lys Lys Gln Glu Lys Met Leu Asp

130

135

<210> 34  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 34

Lys Lys Lys Asp Lys Val Lys Lys Gly Gly Pro Gly Ser Glu Cys Ala  
 1 5 10 15  
 Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser Ser Lys Asp Cys Gly Val  
 20 25 30  
 Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln Thr Gln Arg Ile Arg Cys  
 35 40 45  
 Arg Val Pro Cys Asn Trp Lys Lys Glu Phe Gly Ala Asp Cys Lys Tyr  
 50 55 60  
 Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Gly Thr Gly Thr Lys Val  
 65 70 75 80  
 Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr Asn Ala Gln Cys Gln Glu  
 85 90 95  
 Thr Ile Arg Val Thr Lys Pro Cys Thr Pro Lys Thr Lys Ala Lys Ala  
 100 105 110  
 Lys Ala Lys Lys Gly Lys Gly Lys Asp  
 115 120

<210> 35  
 <211> 43  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 35

Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn Thr Ala  
 1 5 10 15  
 Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn Ala Glu  
 20 25 30  
 Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys  
 35 40

<210> 36  
 <211> 54  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 36

Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn  
 1 5 10 15



Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn  
 20 25 30

Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu  
 35 40 45

Thr Lys Pro Lys Pro Gln  
 50

<210> 37  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<400> 37

Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn  
 1 5 10 15

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn  
 20 25 30

Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu  
 35 40 45

Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys Lys Lys Lys Lys Glu Gly  
 50 55 60

Lys Lys Gln Glu Lys Met Leu Asp  
 65 70

<210> 38  
 <211> 80  
 <212> PRT  
 <213> Homo sapiens

<400> 38

Cys Gly Glu Trp Thr Trp Gly Pro Cys Ile Pro Asn Ser Lys Asp Cys  
 1 5 10 15

Gly Leu Gly Thr Arg Glu Gly Thr Cys Lys Gln Glu Thr Arg Lys Leu  
 20 25 30

Lys Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly Ala Asp Cys  
 35 40 45

Lys Tyr Lys Phe Glu Ser Trp Gly Glu Cys Asp Ala Asn Thr Gly Leu  
 50 55 60

Lys Thr Arg Ser Gly Thr Leu Lys Lys Ala Leu Tyr Asn Ala Asp Cys  
 65 70 75 80

<210> 39  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 39

Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly  
 1 5 10 15

Glu Trp Gln Trp Ser  
 20

<210> 40  
 <211> 16  
 <212> PRT  
 <213> Homo sapiens

<400> 40

Ser Lys Lys Lys Lys Lys Glu Gly Lys Lys Gln Glu Lys Met Leu Asp  
 1 5 10 15

<210> 41  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<400> 41

Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Gly Thr  
 1 5 10 15

Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr Asn Ala  
 20 25 30

Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro Lys Thr  
 35 40 45

Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp  
 50 55 60

<210> 42  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 42

Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Gly Thr Gly Thr  
 1 5 10 15

Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr Asn Ala Gln Cys  
 20 25 30

Gln Glu Thr Ile Arg Val Thr Lys Pro Cys  
 35 40

<210> 43  
 <211> 32  
 <212> PRT  
 <213> Homo sapiens

<400> 43

Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala  
1 5 10 15

Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala  
20 25 30

<210> 44

<211> 20

<212> PRT

<213> Homo sapiens

<400> 44

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala  
1 5 10 15

Leu Thr Ser Ala  
20

<210> 45

<211> 139

<212> PRT

<213> Homo sapiens

<400> 45

Phe Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys  
1 5 10 15

Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp  
20 25 30

Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala  
35 40 45

Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr  
50 55 60

Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn  
65 70 75 80

Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr  
85 90 95

Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys  
100 105 110

Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys  
115 120 125

Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser  
130 135

<210> 46

<211> 15

<212> PRT

<213> Homo sapiens

<400> 46

Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys  
 1 5 10 15

<210> 47  
 <211> 8  
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<400> 47

Lys Lys Asn Gly Ser Cys Lys Arg  
 1 5

<210> 48  
 <211> 13  
 <212> PRT  
 <213> Artificial sequence

<220>  
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<220>  
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 <222> (5)..(5)  
 <223> "Xaa" may be between 5 and 7 of any amino acids

<220>  
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 <223> "Xaa" may be any amino acid

<400> 48

Arg Leu Tyr Cys Xaa Leu Xaa Xaa Xaa Pro Asp Gly Arg  
 1 5 10

<210> 49  
 <211> 4  
 <212> PRT  
 <213> Homo sapiens

<400> 49

Ile Ser Ser Lys  
 1

<210> 50  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<400> 50

Lys Lys Pro Lys Leu  
 1 5

<210> 51  
 <211> 535  
 <212> PRT  
 <213> Homo sapiens

<400> 51

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Met Leu Gly Pro Cys Met Leu Leu Leu Leu Leu Leu Leu Gly Leu Arg
1                               10                      15

Leu Gln Leu Ser Leu Gly Ile Ile Pro Val Glu Glu Glu Asn Pro Asp
20                        25                      30

Phe Trp Asn Arg Glu Ala Ala Glu Ala Leu Gly Ala Ala Lys Lys Leu
35                        40                      45

Gln Pro Ala Gln Thr Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp
50                        55                      60

Gly Met Gly Val Ser Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln
65                        70                      75                      80

Lys Lys Asp Lys Leu Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe
85                        90                      95

Pro Tyr Val Ala Leu Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro
100                       105                     110

Asp Ser Gly Ala Thr Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn
115                       120                     125

Phe Gln Thr Ile Gly Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn
130                       135                     140

Thr Thr Arg Gly Asn Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys
145                       150                     155                     160

Ala Gly Lys Ser Val Gly Val Val Thr Thr Thr Arg Val Gln His Ala
165                       170                     175

Ser Pro Ala Gly Thr Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser
180                       185                     190

Asp Ala Asp Val Pro Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile
195                       200                     205

Ala Thr Gln Leu Ile Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly
210                       215                     220

Gly Arg Lys Tyr Met Phe Arg Met Gly Thr Pro Asp Pro Glu Tyr Pro
225                       230                     235                     240

Asp Asp Tyr Ser Gln Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val
245                       250                     255

Gln Glu Trp Leu Ala Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg
260                       265                     270

Thr Glu Leu Met Gln Ala Ser Leu Asp Pro Ser Val Thr His Leu Met

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275					280					285					
Gly	Leu	Phe	Glu	Pro	Gly	Asp	Met	Lys	Tyr	Glu	Ile	His	Arg	Asp	Ser
290					295					300					
Thr	Leu	Asp	Pro	Ser	Leu	Met	Glu	Met	Thr	Glu	Ala	Ala	Leu	Arg	Leu
305					310					315					320
Leu	Ser	Arg	Asn	Pro	Arg	Gly	Phe	Phe	Leu	Phe	Val	Glu	Gly	Gly	Arg
			325						330					335	
Ile	Asp	His	Gly	His	His	Glu	Ser	Arg	Ala	Tyr	Arg	Ala	Leu	Thr	Glu
			340					345					350		
Thr	Ile	Met	Phe	Asp	Asp	Ala	Ile	Glu	Arg	Ala	Gly	Gln	Leu	Thr	Ser
		355					360					365			
Glu	Glu	Asp	Thr	Leu	Ser	Leu	Val	Thr	Ala	Asp	His	Ser	His	Val	Phe
	370					375					380				
Ser	Phe	Gly	Gly	Tyr	Pro	Leu	Arg	Gly	Ser	Ser	Ile	Phe	Gly	Leu	Ala
385					390					395					400
Pro	Gly	Lys	Ala	Arg	Asp	Arg	Lys	Ala	Tyr	Thr	Val	Leu	Leu	Tyr	Gly
				405					410					415	
Asn	Gly	Pro	Gly	Tyr	Val	Leu	Lys	Asp	Gly	Ala	Arg	Pro	Asp	Val	Thr
			420					425					430		
Glu	Ser	Glu	Ser	Gly	Ser	Pro	Glu	Tyr	Arg	Gln	Gln	Ser	Ala	Val	Pro
		435					440					445			
Leu	Asp	Glu	Glu	Thr	His	Ala	Gly	Glu	Asp	Val	Ala	Val	Phe	Ala	Arg
	450					455					460				
Gly	Pro	Gln	Ala	His	Leu	Val	His	Gly	Val	Gln	Glu	Gln	Thr	Phe	Ile
465					470					475					480
Ala	His	Val	Met	Ala	Phe	Ala	Ala	Cys	Leu	Glu	Pro	Tyr	Thr	Ala	Cys
				485					490					495	
Asp	Leu	Ala	Pro	Pro	Ala	Gly	Thr	Thr	Asp	Ala	Ala	His	Pro	Gly	Arg
			500					505					510		
Ser	Val	Val	Pro	Ala	Leu	Leu	Pro	Leu	Leu	Ala	Gly	Thr	Leu	Leu	Leu
		515					520					525			
Leu	Glu	Thr	Ala	Thr	Ala	Pro									
	530					535									
<210> 52															
<211> 22															
<212> PRT															
<213> Homo sapiens															
<400> 52															
Met	Leu	Gly	Pro	Cys	Met	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Leu	Arg
1				5						10				15	

Leu Gln Leu Ser Leu Gly  
20

<210> 53  
<211> 29  
<212> PRT  
<213> Homo sapiens  
  
<400> 53

Ala Ala His Pro Gly Arg Ser Val Val Pro Ala Leu Leu Pro Leu Leu  
1 5 10 15

Ala Gly Thr Leu Leu Leu Leu Glu Thr Ala Thr Ala Pro  
20 25

<210> 54  
<211> 108  
<212> PRT  
<213> Homo sapiens  
  
<400> 54

Gly Met Gly Val Ser Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln  
1 5 10 15

Lys Lys Asp Lys Leu Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe  
20 25 30

Pro Tyr Val Ala Leu Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro  
35 40 45

Asp Ser Gly Ala Thr Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn  
50 55 60

Phe Gln Thr Ile Gly Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn  
65 70 75 80

Thr Thr Arg Gly Asn Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys  
85 90 95

Ala Gly Lys Ser Val Gly Val Val Thr Thr Thr Arg  
100 105

<210> 55  
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<223> "Xaa" may be any amino acid

<400> 55

Ala Gln Val Pro Asp Ser Ala Xaa Thr Ala Thr Ala Tyr Leu Cys Gly  
1 5 10 15

Val Lys Ala Asn  
20

<210> 56

<211> 86

<212> PRT

<213> Artificial sequence

<220>

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<222> ()..()

<223> Synthetic

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<222> (7)..(7)

<223> "Xaa" may be any amino acid

<220>

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<222> (30)..(30)

<223> "Xaa" may be any amino acid

<220>

<221> misc\_feature

<222> (33)..(34)

<223> "Xaa" may be any amino acid

<220>

<221> misc\_feature

<222> (36)..(36)

<223> "Xaa" may be any amino acid

<220>

<221> misc\_feature

<222> (39)..(39)

<223> "Xaa" may be any amino acid

<220>

<221> misc\_feature

<222> (41)..(41)

<223> "Xaa" may be any amino acid

<220>

<221> misc\_feature

<222> (44)..(44)

<223> "Xaa" may be any amino acid

<220>

<221> misc\_feature

<222> (47)..(47)

<223> "Xaa" may be any amino acid



<220>  
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 <222> (56)..(57)  
 <223> "Xaa" may be any amino acid

<220>  
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 <223> "Xaa" may be any amino acid

<220>  
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 <222> (78)..(79)  
 <223> "Xaa" may be any amino acid

<220>  
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 <222> (81)..(81)  
 <223> "Xaa" may be any amino acid

<220>  
 <221> misc\_feature  
 <222> (83)..(83)  
 <223> "Xaa" may be any amino acid

<400> 56

Thr Asn Val Ala Lys Asn Xaa Ile Met Phe Leu Gly Asp Gly Met Gly  
 1 5 10 15

Val Ser Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Xaa His His  
 20 25 30

Xaa Xaa Gly Xaa Glu Thr Xaa Leu Xaa Met Asp Xaa Phe Pro Xaa Val  
 35 40 45

Ala Leu Ser Lys Thr Tyr Asn Xaa Xaa Ala Gln Val Pro Asp Ser Ala  
 50 55 60

Xaa Thr Ala Thr Ala Tyr Leu Cys Gly Val Lys Ala Asn Xaa Xaa Thr  
 65 70 75 80

Xaa Gly Xaa Ser Ala Ala  
 85

<210> 57  
 <211> 53  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<220>  
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 <223> "Xaa" may be any amino acid

<220>  
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 <223> "Xaa" may be any amino acid

<220>  
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 <222> (22)..(22)  
 <223> "Xaa" may be any amino acid

<220>  
 <221> misc\_feature  
 <222> (34)..(35)  
 <223> "Xaa" may be any amino acid

<220>  
 <221> misc\_feature  
 <222> (41)..(42)  
 <223> "Xaa" may be any amino acid

<400> 57

Glu Asp Thr Leu Thr Xaa Val Thr Ala Asp His Ser His Val Phe Xaa  
 1 5 10 15

Phe Gly Gly Tyr Thr Xaa Arg Gly Asn Ser Ile Phe Gly Leu Ala Pro  
 20 25 30

Met Xaa Xaa Asp Thr Asp Lys Lys Xaa Xaa Thr Ala Ile Leu Tyr Gly  
 35 40 45

Asn Gly Pro Gly Tyr  
 50

<210> 58  
 <211> 22  
 <212> PRT  
 <213> Homo sapiens

<400> 58

Val Val Pro Ala Leu Leu Pro Leu Leu Ala Gly Thr Leu Leu Leu Leu  
 1 5 10 15

Glu Thr Ala Thr Ala Pro  
 20

<210> 59  
 <211> 154  
 <212> PRT  
 <213> Homo sapiens

<400> 59

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly

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      20              25              30
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
  35              40              45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
  50              55              60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
  65              70              75              80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
  85              90              95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
  100              105              110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
  115              120              125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
  130              135              140

Arg Gly Lys Gly Cys Asp Lys Pro Arg Arg
  145              150

<210> 60
<211> 162
<212> PRT
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 60

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
  1              5              10              15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
  20              25              30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
  35              40              45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
  50              55              60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
  65              70              75              80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
  85              90              95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
  100              105              110

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Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val  
 130 135 140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Cys Asp Lys Pro  
 145 150 155 160

Arg Arg

<210> 61  
 <211> 150  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 61

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Lys Lys  
 130 135 140

Cys Asp Lys Pro Arg Arg  
 145 150

<210> 62  
 <211> 154  
 <212> PRT  
 <213> Artificial sequence

<220>

<221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 62

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Lys Lys  
 130 135 140

Lys Lys Lys Lys Cys Asp Lys Pro Arg Arg  
 145 150

<210> 63  
 <211> 7  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 63

Gly Gly Gly Gly Ser Ser Ser  
 1 5

<210> 64  
 <211> 4  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()

<223> Synthetic

<400> 64

Ile Glu Gly Arg  
1

<210> 65

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<221> misc\_feature

<222> ()..()

<223> Synthetic

<400> 65

Pro Gly Ile Ser Gly Gly Gly Gly Gly  
1 5

<210> 66

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<221> misc\_feature

<222> ()..()

<223> Synthetic

<400> 66

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

<210> 67

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<221> misc\_feature

<222> ()..()

<223> Synthetic

<400> 67

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Lys Glu Phe  
1 5 10

<210> 68

<211> 26

<212> PRT

<213> Homo sapiens

<400> 68

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15

Val Leu His His Ala Lys Trp Ser Gln Ala  
 20 25

<210> 69  
 <211> 33  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 69  
 cgcggaatcca ccatgaactt tctgctgtct tgg 33

<210> 70  
 <211> 39  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 70  
 ctaaattggtt tctcttcctc cccgcctcgg cttgtcaca 39

<210> 71  
 <211> 39  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 71  
 tgtgacaagc ctgaggcggg aggaagagaa accatttag 39

<210> 72  
 <211> 28  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 72  
 cgcggaatcct caaaaatcta aaggtcga 28

<210> 73

<211> 1107  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 73  
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 gtctatcagc gcagctactg ccatccaatc gagaccctgg tggacatctt ccaggagtac 120  
 cctgatgaga tcgagtacat cttcaagcca atgaactttc tgctgtcttg ggtgcattgg 180  
 agccttgcc t gctgtctcta cctccaccat gccaaagtggc cccagtcctg tgtgcccctg 240  
 atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300  
 aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360  
 agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420  
 aaatgtgaca agccgaggcg ggaggaagag aaaccattta gagactgtgc agatgtatat 480  
 caagctgggt ttaataaaaag tggaaatctac actatttata ttaataatat gccagaaccc 540  
 aaaaagggtg tttgcaatat ggatgtcaat gggggagggt ggactgtaat acaacatcgt 600  
 gaagatggaa gtctagattt ccaaagaggc tggaaaggaat ataaaatggg ttttggaat 660  
 ccctccggtg aatattggct ggggaatgag tttatTTTTg ccattaccag tcagaggcag 720  
 tacatgctaa gaattgagtt aatggactgg gaagggaacc gagcctattc acagtatgac 780  
 agattccaca taggaaatga aaagcaaac tataggttgt atttaaaagg tcacactggg 840  
 acagcaggaa aacagagcag cctgatctta cacggtgctg atttcagcac taaagatgct 900  
 gataatgaca actgtatgtg caaatgtgcc ctcatgttaa caggaggatg gtggtttgat 960  
 gcttgtggcc cctccaatct aaatggaatg ttctatactg cgggacaaaa ccatggaaaa 1020  
 ctgaatggga taaagtggca ctacttcaaa gggcccagtt actccttacg ttccacaact 1080  
 atgatgattc gacctttaga tttttga 1107

<210> 74  
 <211> 368  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 74



Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15  
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30  
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45  
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60  
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80  
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
 85 90 95  
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110  
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125  
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys  
 130 135 140  
 Pro Arg Arg Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp Val Tyr  
 145 150 155 160  
 Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile Asn Asn  
 165 170 175  
 Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly  
 180 185 190  
 Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln  
 195 200 205  
 Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu  
 210 215 220  
 Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln  
 225 230 235 240  
 Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr  
 245 250 255  
 Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg  
 260 265 270  
 Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu  
 275 280 285  
 Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn  
 290 295 300  
 Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp



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<400> 78
atgaactttc tgctgtcttg ggtgcattgg agccttgcct tgctgctcta cctccaccat      60
gccaagtggg cccaggctgc acccatggca gaaggaggag gccagaatca tcacgaagtg      120
gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac      180
atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg      240
atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc      300
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg      360
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa      420
aaatgtgaca agccgaggcg gcaatttggc gcggagtgca aataccagtt ccaggcctgg      480
ggagaatgtg acctgaacac agccctgaag accagaactg gaagtctgaa gcgagccctg      540
cacaatgccg aatgccagaa gactgtcacc atctccaagc cctgtggcaa actgaccaag      600
cccaaacctc aagcagaatc taagaagaag aaaaaggaag gcaagaaaca ggagaagatg      660
ctggattaa                                     669

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<210> 79
<211> 222
<212> PRT
<213> Artificial sequence

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<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

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<400> 79

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Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1              5              10              15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
              20              25              30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
              35              40              45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50              55              60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65              70              75              80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
              85              90              95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
              100              105              110

```

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys  
 130 135 140

Pro Arg Arg Gln Phe Gly Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp  
 145 150 155 160

Gly Glu Cys Asp Leu Asn Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu  
 165 170 175

Lys Arg Ala Leu His Asn Ala Glu Cys Gln Lys Thr Val Thr Ile Ser  
 180 185 190

Lys Pro Cys Gly Lys Leu Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys  
 195 200 205

Lys Lys Lys Lys Glu Gly Lys Lys Gln Glu Lys Met Leu Asp  
 210 215 220

<210> 80  
 <211> 37  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 80  
 tgcagtcggc tccaaactcc cgctcggt tgtcaca

37

<210> 81  
 <211> 37  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 81  
 tgtgacaagc cgaggcggga gtttggagcc gactgca

37

<210> 82  
 <211> 27  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 82  
 cgcgatccc tagtcctttc ccttccc

27

<210> 83  
 <211> 639  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 83  
 atgaactttc tgctgtcttg ggtgcattgg agccttgcct tgctgtctta cctccaccat 60  
 gccaaagtggc cccaggctgc acccatggca gaaggaggag ggcagaatca tcacgaagtg 120  
 gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctgggtggac 180  
 atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg 240  
 atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300  
 aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360  
 agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420  
 aaatgtgaca agccgaggcg ggagtttggg gccgactgca agtacaagtt tgagaactgg 480  
 ggtgcgtgtg atggggggcac aggcacaaaa gtccgccaag gcaccctgaa gaaggcgcg 540  
 tacaatgctc agtgccagga gaccatccgc gtcaccaagc cctgcacccc caagacaaaa 600  
 gcaaaggcca aagccaagaa agggaaggga aaggactag 639

<210> 84  
 <211> 212  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 84

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15  
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30  
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45  
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60  
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu



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<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 87
cgcgatcct tagtggagg tggtgggg                                     28

<210> 88
<211> 1116
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 88
atgaactttc tgctgtcttg ggtgcattgg agccttgctt tgctgtctta cctccaccat      60
gccaagtggg cccaggctgc acccatggca gaaggaggag ggcagaatca tcacgaagtg      120
gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctgggtggac      180
atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccttg      240
atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc      300
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg      360
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa      420
aaatgtgaca agccgaggcg gaagccgtcg ggcccatgga gagactgcct gcaggccctg      480
gaggatggcc acgacaccag ctccatctac ctgggtgaagc cggagaacac caaccgcctc      540
atgcagggtg ggtgcgacca gagacacgac cccggggggct ggaccgtcat ccagagacgc      600
ctggatggct ctgttaactt cttcaggaac tgggagacgt acaagcaagg gtttggaac      660
attgatggcg aatactggct gggcctggag aacatttact ggctgacgaa ccaaggcaac      720
tacaaactcc tggtgaccat ggaggactgg tccggccgca aagtctttgc agaatacgcc      780
agtttccgcc tggaaacctga gagcgagtat tataagctgc ggctggggcg ctaccatggc      840
aatgcgggtg actcctttac atggcacaac ggcaagcagt tcaccaccct ggacagagat      900
catgatgtct acacaggaaa ctgtgcccac taccagaagg gaggctgggtg gtataacgcc      960
tgtgccact ccaacctcaa cggggtctgg taccgcgggg gccattaccg gagccgctac     1020
caggacggag tctactgggc tgagttccga ggaggctctt actcactcaa gaaagtgggtg     1080
atgatgatcc gaccgaaccc caacaccttc cactaa                               1116

<210> 89

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<211> 371  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 89

Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala	Leu	Leu	Leu	1	5	10	15
Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala	Glu	Gly	20	25	30	
Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	Val	Tyr	Gln	35	40	45	
Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	Ile	Phe	Gln	Glu	50	55	60	
Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	Cys	Val	Pro	Leu	65	70	75	80
Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	Glu	Cys	Val	Pro	85	90	95	
Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His	100	105	110	
Gln	Gly	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Asn	Lys	Cys	115	120	125	
Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	Lys	Cys	Asp	Lys	130	135	140	
Pro	Arg	Arg	Lys	Pro	Ser	Gly	Pro	Trp	Arg	Asp	Cys	Leu	Gln	Ala	Leu	145	150	155	160
Glu	Asp	Gly	His	Asp	Thr	Ser	Ser	Ile	Tyr	Leu	Val	Lys	Pro	Glu	Asn	165	170	175	
Thr	Asn	Arg	Leu	Met	Gln	Val	Trp	Cys	Asp	Gln	Arg	His	Asp	Pro	Gly	180	185	190	
Gly	Trp	Thr	Val	Ile	Gln	Arg	Arg	Leu	Asp	Gly	Ser	Val	Asn	Phe	Phe	195	200	205	
Arg	Asn	Trp	Glu	Thr	Tyr	Lys	Gln	Gly	Phe	Gly	Asn	Ile	Asp	Gly	Glu	210	215	220	
Tyr	Trp	Leu	Gly	Leu	Glu	Asn	Ile	Tyr	Trp	Leu	Thr	Asn	Gln	Gly	Asn	225	230	235	240
Tyr	Lys	Leu	Leu	Val	Thr	Met	Glu	Asp	Trp	Ser	Gly	Arg	Lys	Val	Phe	245	250	255	



Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys  
260 265 270

Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp  
275 280 285

His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp His Asp Val Tyr  
290 295 300

Thr Gly Asn Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala  
305 310 315 320

Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr  
325 330 335

Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly  
340 345 350

Ser Tyr Ser Leu Lys Lys Val Val Met Met Ile Arg Pro Asn Pro Asn  
355 360 365

Thr Phe His  
370

<210> 90  
<211> 36  
<212> DNA  
<213> Artificial sequence

<220>  
<221> misc\_feature  
<222> ()..()  
<223> Synthetic

<400> 90  
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36

<210> 91  
<211> 36  
<212> DNA  
<213> Artificial sequence

<220>  
<221> misc\_feature  
<222> ()..()  
<223> Synthetic

<400> 91  
tgtgacaagc cgaggcgat caatgaagga ccattc

36

<210> 92  
<211> 29  
<212> DNA  
<213> Artificial sequence

<220>  
<221> misc\_feature  
<222> ()..()  
<223> Synthetic

<400> 92  
cgcggtacct cagtcaatag gcttgatca 29

<210> 93  
<211> 1104  
<212> DNA  
<213> Artificial sequence

<220>  
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<222> ()..()  
<223> Synthetic

<400> 93  
atgaactttc tgctgtcttg ggtgcattgg agccttgcct tgctgctcta cctccaccat 60  
gccaagtggg cccaggctgc acccatggca gaaggaggag ggcagaatca tcacgaagtg 120  
gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctgggtggac 180  
atcttcagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg 240  
atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300  
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360  
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420  
aaatgtgaca agccgaggcg gatcaatgaa ggaccattca aagactgtca gcaagcaaaa 480  
gaagctgggc attcgggtcag tgggatttat atgattaaac ctgaaaacag caatggacca 540  
atgcagttat ggtgtgaaaa cagtttggac cctggggggt ggactgttat tcagaaaaga 600  
acagacggct ctgtcaactt cttcagaaat tgggaaaatt ataagaaagg gtttggaaaac 660  
attgacggag aatactggct tggactggaa aatatctata tgcttagcaa tcaagataat 720  
tacaagttat tgattgaatt agaagactgg agtgataaaa aagtctatgc agaatacagc 780  
agctttcgtc tggaaacctga aagtgaattc tatagactgc gcctgggaac ttaccagggg 840  
aatgcagggg attctatgat gtggcataat ggtaaacaat tcaccacact ggacagagat 900  
aaagatatgt atgcaggaaa ctgcgcccac tttcataaag gaggctgggtg gtacaatgcc 960  
tgtgcacatt ctaacctaaa tggagtatgg tacagaggag gccattacag aagcaagcac 1020  
caagatggaa ttttctgggc cgaatacaga ggcgggtcat actccttaag agcagttcag 1080  
atgatgatca agcctattga ctga 1104

<210> 94  
<211> 367  
<212> PRT  
<213> Artificial sequence

<220>

&lt;221&gt; misc\_feature

&lt;222&gt; ()..()

&lt;223&gt; Synthetic

&lt;400&gt; 94

```

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1          5          10          15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
          20          25          30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
          35          40          45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50          55          60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65          70          75          80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
          85          90          95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
          100          105          110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
          115          120          125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
          130          135          140

Pro Arg Arg Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys
          145          150          155          160

Glu Ala Gly His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn
          165          170          175

Ser Asn Gly Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro Gly
          180          185          190

Gly Trp Thr Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe
          195          200          205

Arg Asn Trp Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu
          210          215          220

Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn
          225          230          235          240

Tyr Lys Leu Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr
          245          250          255

Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg
          260          265          270

Leu Arg Leu Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp
          275          280          285

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His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr  
 290 295 300

Ala Gly Asn Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala  
 305 310 315 320

Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr  
 325 330 335

Arg Ser Lys His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly  
 340 345 350

Ser Tyr Ser Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp  
 355 360 365

<210> 95  
 <211> 1387  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<220>  
 <221> misc\_feature  
 <222> (1201)..(1219)  
 <223> "n" may be any nucleotide

<220>  
 <221> misc\_feature  
 <222> (1295)..(1324)  
 <223> "n" may be any nucleotide

<400> 95  
 atgtggcaga ttgttttctt tactctgagc tgtgatcttg tcttggccgc agcctataac 60  
 aactttcggg agagcatgga cagcatagga aagaagcaat atcaggtcca gcatgggtcc 120  
 tgcagctaca ctttcctcct gccagagatg gacaactgcc gctcttcctc cagcccctac 180  
 gtgtccaatg ctgtgcagag ggacgcgccg ctccaatacg atgactcggg gcagaggctg 240  
 caagtgcctg agaacatcat ggaaaacaac actcagtggc taatgaaggt agagaatata 300  
 tcccaggaca acatgaagaa agaaatggta gagatacagc agaatgcagt acagaaccag 360  
 acggctgtga tgatagaaat agggacaaac ctgttgaacc aaacagcgga gcaaacgcgg 420  
 aagttaactg atgtggaagc ccaagtatta aatcagacca cgagacttga acttcagctc 480  
 ttggaacact ccctctcgac aaacaaattg gaaaaacaga ttttggacca gaccagtga 540  
 ataaacaaat tgcaagataa gaacagtttc ctagaaaaga aggtgctagc tatggaagac 600  
 aagcacatca tccaactaca gtcaataaaa gaagagaaaag atcagctaca ggtgttagta 660

```

tccaagcaga attccatcat tgaagaactc gaaaaaaaaa tagtgactgc cacgggtgaat 720
aattcagttc ttcagaagca gcaacatgat ctcatggaga cagttaataa cttactgact 780
atgatgtcca catcaaacgc agctaaggac cccactgttg ctaaagaaga acaaatcagc 840
ttcagagact gtgctgaagt attcaaatac ggacacacca cgaatggcat ctacacgtta 900
acattcccta attctacaga agagatcaag gcctactgtg acatggaagc tggaggaggc 960
gggtggacaa ttattcagcg acgtgaggat ggacagcgtg catttcagag gacttggaaa 1020
gaatataaag tgggatttgg taacctctca gaaaaatatt ggctgggaaa tgagtttgtt 1080
tcgcaactga ctaatcagca acgctatgtg cttaaaatac accttaaaga ctgggaaggg 1140
aatgaggctt actcattgta tgaacatttc tatctctcaa gtgaagaact caattatagg 1200
nnnnnnnnnn nnnnnnnnng gcaatgattt tagcacaagg gatggagcca ccgncanatg 1260
tatttgcaaa tggtcacaaa tgctaacagn aggtnnnnnn nnnnnnnnnn nnnnnnnnnn 1320
nnnntactgg aaaggctcag gctattcgct caaggccaca accatgatga tccgaccagc 1380
agatttc 1387

```

```

<210> 96
<211> 360
<212> PRT
<213> Artificial sequence

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<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

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```

<220>
<221> misc_feature
<222> (269)..(272)
<223> "Xaa" may be any amino acid

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<400> 96

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```

Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala
1          5          10          15
Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys
20          25          30
Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
35          40          45
Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
50          55          60
Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
65          70          75          80
Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys

```

85										90					95				
Leu	Glu	Asn	Ile	Ser	Gln	Asp	Asn	Met	Lys	Lys	Glu	Met	Val	Glu	Ile				
			100					105							110				
Gln	Gln	Asn	Ala	Val	Gln	Asn	Gln	Thr	Ala	Val	Met	Ile	Glu	Ile	Gly				
		115					120					125							
Thr	Asn	Leu	Leu	Asn	Gln	Thr	Ala	Glu	Gln	Thr	Arg	Lys	Leu	Thr	Asp				
	130					135					140								
Val	Glu	Ala	Gln	Val	Ser	Asn	Ala	Thr	Thr	Arg	Leu	Glu	Leu	Gln	Leu				
	145				150						155				160				
Leu	Glu	His	Ser	Leu	Ser	Thr	Asn	Lys	Leu	Glu	Lys	Gln	Ile	Leu	Asp				
			165						170					175					
Gln	Thr	Ser	Glu	Ile	Asn	Lys	Leu	Gln	Asp	Lys	Asn	Ser	Phe	Leu	Glu				
		180					185						190						
Lys	Lys	Val	Leu	Ala	Met	Glu	Asp	Lys	His	Ile	Ile	Gln	Leu	Gln	Ser				
		195					200					205							
Ile	Lys	Glu	Glu	Lys	Asp	Gln	Leu	Gln	Val	Leu	Val	Ser	Lys	Gln	Asn				
	210					215					220								
Ser	Ile	Ile	Glu	Glu	Leu	Glu	Lys	Lys	Ile	Val	Thr	Ala	Thr	Val	Asn				
	225				230						235				240				
Asn	Ser	Val	Leu	Gln	Lys	Gln	Gln	His	Asp	Leu	Met	Glu	Thr	Val	Asn				
			245					250						255					
Asn	Leu	Leu	Thr	Met	Met	Ser	Thr	Ser	Asn	Cys	Lys	Xaa	Xaa	Xaa	Xaa				
		260						265				270							
Val	Ala	Lys	Glu	Glu	Gln	Ile	Ser	Phe	Arg	Asp	Cys	Ala	Glu	Val	Phe				
		275					280					285							
Lys	Ser	Gly	His	Thr	Thr	Asn	Gly	Ile	Tyr	Thr	Leu	Met	Trp	Gln	Ile				
	290					295					300								
Val	Phe	Phe	Thr	Leu	Ser	Cys	Asp	Leu	Val	Leu	Ala	Ala	Ala	Tyr	Asn				
	305				310						315				320				
Asn	Phe	Arg	Lys	Ser	Met	Asp	Ser	Ile	Gly	Lys	Lys	Gln	Tyr	Gln	Val				
			325						330					335					
Gln	His	Gly	Ser	Cys	Ser	Tyr	Thr	Phe	Leu	Leu	Pro	Glu	Met	Asp	Asn				
		340						345					350						
Cys	Arg	Ser	Ser	Ser	Ser	Pro	Tyr												
		355					360												

&lt;210&gt; 97

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

<221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 97

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Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1          5          10          15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
          20          25          30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
          35          40          45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50          55          60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65          70          75          80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
          85          90          95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
          100          105          110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115          120          125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
130          135          140

Pro Arg Arg Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val
145          150          155          160

Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu
          165          170          175

Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro
          180          185          190

Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser
195          200          205

Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn
210          215          220

Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln
225          230          235          240

Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln
          245          250          255

Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp
          260          265          270

Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp
275          280          285

```

Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr  
 290 295 300

Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe  
 305 310 315 320

Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro  
 325 330 335

Leu Asp Phe

<210> 98  
 <211> 361  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 98  
 gtccaatgct gtgcagaggg acgcgccgct cgaatacgat gactcgggtgc agaggctgca 60  
 agtgctggag aacatcatgg aaaacaacac tcagtggcta atgaaggtag agaatatatc 120  
 ccaggacaac atgaagaaaag aaatggtaga gatacagcag aatgcagtac agaaccagac 180  
 ggctgtgatg atagaaatag ggacaaacct gttgaaccaa acagcggagc aaacgcggaa 240  
 gttaactgat gtggaagccc aagtattaaa tcagaccacg agacttgaac ttcagctctt 300  
 ggaacactcc ctctcgacaa acaaattgga aaaacagatt ttggaccaga ccagtgaaat 360  
 a 361

<210> 99  
 <211> 123  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 99

Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser  
 1 5 10 15

Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln  
 20 25 30

Trp Leu Met Lys Leu Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu  
 35 40 45

Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met



50                                      55                                      60  
 Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg  
 65                                      70                                      75                                      80  
 Lys Leu Thr Asp Val Glu Ala Gln Val Ser Asn Ala Thr Thr Arg Leu  
 85                                      90                                      95  
 Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys  
 100                                      105                                      110  
 Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys  
 115                                      120  
 <210> 100  
 <211> 462  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic  
 <400> 100  
 Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser  
 1                                      5                                      10                                      15  
 Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln  
 20                                      25                                      30  
 Trp Leu Met Lys Leu Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu  
 35                                      40                                      45  
 Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met  
 50                                      55                                      60  
 Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg  
 65                                      70                                      75                                      80  
 Lys Leu Thr Asp Val Glu Ala Gln Val Ser Asn Ala Thr Thr Arg Leu  
 85                                      90                                      95  
 Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys  
 100                                      105                                      110  
 Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys Met Asn Phe Leu Leu  
 115                                      120                                      125  
 Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu Tyr Leu His His Ala  
 130                                      135                                      140  
 Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly Gly Gly Gln Asn His  
 145                                      150                                      155                                      160  
 His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His  
 165                                      170                                      175

Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile  
 180 185 190  
 Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly  
 195 200 205  
 Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn  
 210 215 220  
 Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile  
 225 230 235 240  
 Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys  
 245 250 255  
 Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys Pro Arg Arg Met Pro  
 260 265 270  
 Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly Gly Trp  
 275 280 285  
 Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly  
 290 295 300  
 Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp  
 305 310 315 320  
 Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met  
 325 330 335  
 Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln  
 340 345 350  
 Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr  
 355 360 365  
 Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu  
 370 375 380  
 His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn Cys Met  
 385 390 395 400  
 Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys  
 405 410 415  
 Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln Asn His  
 420 425 430  
 Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr  
 435 440 445  
 Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe  
 450 455 460  
 <210> 101  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 101

Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly  
 1 5 10 15  
 His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn Arg  
 20 25 30  
 Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr  
 35 40 45  
 Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp  
 50 55 60  
 Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu  
 65 70 75 80  
 Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu  
 85 90 95  
 Leu Val Thr Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr  
 100 105 110  
 Ala Ser Phe Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu  
 115 120 125  
 Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly  
 130 135 140  
 Lys Gln Phe Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn  
 145 150 155 160  
 Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His  
 165 170 175  
 Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg  
 180 185 190  
 Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser  
 195 200 205  
 Leu Lys Lys Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His  
 210 215 220

&lt;210&gt; 102

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 102

Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys Glu Ala Gly  
 1 5 10 15  
 His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn Ser Asn Gly  
 20 25 30  
 Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro Gly Gly Trp Thr  
 35 40 45

Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe Arg Asn Trp  
 50 55 60  
 Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu  
 65 70 75 80  
 Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn Tyr Lys Leu  
 85 90 95  
 Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr Ala Glu Tyr  
 100 105 110  
 Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg Leu Arg Leu  
 115 120 125  
 Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp His Asn Gly  
 130 135 140  
 Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr Ala Gly Asn  
 145 150 155 160  
 Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His  
 165 170 175  
 Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys  
 180 185 190  
 His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly Ser Tyr Ser  
 195 200 205  
 Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp  
 210 215 220  
 <210> 103  
 <211> 371  
 <212> PRT  
 <213> Artificial sequence  
 <220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic  
 <400> 103  
 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1 5 10 15  
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
 20 25 30  
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45  
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60  
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu

60

[illegible]

<210> 104  
 <211> 367  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 104

Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala	Leu	Leu	Leu	1	5	10	15
Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	Ala	Glu	Gly	20	25	30	
Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	Asp	Val	Tyr	Gln	35	40	45	
Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	Ile	Phe	Gln	Glu	50	55	60	
Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	Cys	Val	Pro	Leu	65	70	75	80
Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	Glu	Cys	Val	Pro	85	90	95	
Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His	100	105	110	
Gln	Gly	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Asn	Lys	Cys	115	120	125	
Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	Lys	Cys	Asp	Lys	130	135	140	
Pro	Arg	Arg	Ile	Asn	Glu	Gly	Pro	Phe	Lys	Asp	Cys	Gln	Gln	Ala	Lys	145	150	155	160
Glu	Ala	Gly	His	Ser	Val	Ser	Gly	Ile	Tyr	Met	Ile	Lys	Pro	Glu	Asn	165	170	175	
Ser	Asn	Gly	Pro	Met	Gln	Leu	Trp	Cys	Glu	Asn	Ser	Leu	Asp	Pro	Gly	180	185	190	
Gly	Trp	Thr	Val	Ile	Gln	Lys	Arg	Thr	Asp	Gly	Ser	Val	Asn	Phe	Phe	195	200	205	
Arg	Asn	Trp	Glu	Asn	Tyr	Lys	Lys	Gly	Phe	Gly	Asn	Ile	Asp	Gly	Glu	210	215	220	
Tyr	Trp	Leu	Gly	Leu	Glu	Asn	Ile	Tyr	Met	Leu	Ser	Asn	Gln	Asp	Asn	225	230	235	240
Tyr	Lys	Leu	Leu	Ile	Glu	Leu	Glu	Asp	Trp	Ser	Asp	Lys	Lys	Val	Tyr	245	250	255	

Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg  
260 265 270

Leu Arg Leu Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp  
275 280 285

His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr  
290 295 300

Ala Gly Asn Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala  
305 310 315 320

Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr  
325 330 335

Arg Ser Lys His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly  
340 345 350

Ser Tyr Ser Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp  
355 360 365

<210> 105

<211> 53

<212> PRT

<213> Homo sapiens

<400> 105

Lys Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu  
1 5 10 15

Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile  
20 25 30

Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr  
35 40 45

Asp Val Glu Ala Gln  
50

<210> 106

<211> 105

<212> PRT

<213> Homo sapiens

<400> 106

His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg  
1 5 10 15

Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly  
20 25 30

Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro  
35 40 45

Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu  
50 55 60

Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln  
65 70 75 80

Gln Gln Arg His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln  
85 90 95

Ser Gln Phe Gly Leu Leu Asp His Lys  
100 105

<210> 107

<211> 192

<212> PRT

<213> Homo sapiens

<400> 107

Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr Ile Lys  
1 5 10 15

Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp Val Leu Ser  
20 25 30

Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val Val Asp Val Asp  
35 40 45

Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg Lys Glu Ser Arg Asn  
50 55 60

Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu Ile  
65 70 75 80

Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu Ser Gln Leu Glu Asn Lys  
85 90 95

Ile Leu Asn Val Thr Thr Glu Met Leu Lys Met Ala Thr Arg Tyr Arg  
100 105 110

Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr Asp Leu Val Asn Asn Gln  
115 120 125

Ser Val Met Ile Thr Leu Leu Glu Glu Gln Cys Leu Arg Ile Phe Ser  
130 135 140

Arg Gln Asp Thr His Val Ser Pro Pro Leu Val Gln Val Val Pro Gln  
145 150 155 160

His Ile Pro Asn Ser Gln Gln Tyr Thr Pro Gly Leu Leu Gly Gly Asn  
165 170 175

Glu Ile Gln Arg Asp Pro Gly Tyr Pro Arg Asp Leu Met Pro Pro Pro  
180 185 190

<210> 108

<211> 196

<212> PRT

<213> Homo sapiens

<400> 108



Pro Tyr Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp  
 1 5 10 15  
 Asp Ser Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn  
 20 25 30  
 Thr Gln Trp Leu Met Lys Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys  
 35 40 45  
 Lys Glu Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala  
 50 55 60  
 Val Met Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln  
 65 70 75 80  
 Thr Arg Lys Leu Thr Asp Val Glu Ala Gln Val Leu Asn Gln Thr Thr  
 85 90 95  
 Arg Leu Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu  
 100 105 110  
 Glu Lys Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp  
 115 120 125  
 Lys Asn Ser Phe Leu Glu Lys Lys Val Leu Ala Met Glu Asp Lys His  
 130 135 140  
 Ile Ile Gln Leu Gln Ser Ile Lys Glu Glu Lys Asp Gln Leu Gln Val  
 145 150 155 160  
 Leu Val Ser Lys Gln Asn Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile  
 165 170 175  
 Val Thr Ala Thr Val Asn Asn Ser Val Leu Gln Lys Gln Gln His Asp  
 180 185 190  
 Leu Met Glu Thr  
 195

<210> 109  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 109

His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg  
 1 5 10 15  
 Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly  
 20 25 30  
 Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro  
 35 40 45  
 Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu  
 50 55 60

LVM 205654

65

Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln  
65 70 75 80

Gln Gln Arg His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln  
85 90 95

Ser Gln Phe Gly Leu Leu Asp His Lys  
100 105

<210> 110

<211> 192

<212> PRT

<213> Homo sapiens

<400> 110

Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr Ile Lys  
1 5 10 15

Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp Val Leu Ser  
20 25 30

Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val Val Asp Val Asp  
35 40 45

Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg Lys Glu Ser Arg Asn  
50 55 60

Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu Ile  
65 70 75 80

Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu Ser Gln Leu Glu Asn Lys  
85 90 95

Ile Leu Asn Val Thr Thr Glu Met Leu Lys Met Ala Thr Arg Tyr Arg  
100 105 110

Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr Asp Leu Val Asn Asn Gln  
115 120 125

Ser Val Met Ile Thr Leu Leu Glu Glu Gln Cys Leu Arg Ile Phe Ser  
130 135 140

Arg Gln Asp Thr His Val Ser Pro Pro Leu Val Gln Val Val Pro Gln  
145 150 155 160

His Ile Pro Asn Ser Gln Gln Tyr Thr Pro Gly Leu Leu Gly Gly Asn  
165 170 175

Glu Ile Gln Arg Asp Pro Gly Tyr Pro Arg Asp Leu Met Pro Pro Pro  
180 185 190

<210> 111

<211> 135

<212> PRT

<213> Homo sapiens

<400> 111

Asp Ala Ser Thr Ile Lys Asp Met Ile Thr Arg Met Asp Leu Glu Asn  
 1 5 10 15  
 Leu Lys Asp Val Leu Ser Arg Gln Lys Arg Glu Ile Asp Val Leu Gln  
 20 25 30  
 Leu Val Val Asp Val Asp Gly Asn Ile Val Asn Glu Val Lys Leu Leu  
 35 40 45  
 Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met  
 50 55 60  
 Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu  
 65 70 75 80  
 Ser Gln Leu Glu Asn Lys Ile Leu Asn Val Thr Thr Glu Met Leu Lys  
 85 90 95  
 Met Ala Thr Arg Tyr Arg Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr  
 100 105 110  
 Asp Leu Val Asn Asn Gln Ser Val Met Ile Thr Leu Leu Glu Glu Gln  
 115 120 125  
 Cys Leu Arg Ile Phe Ser Arg  
 130 135

<210> 112  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 112

Glu Leu Glu Leu Leu Asn Asn Glu Leu Leu Lys Gln Lys Arg Gln Ile  
 1 5 10 15  
 Glu Thr Leu Gln Gln Leu Val Glu Val Asp Gly Gly Ile Val Ser Glu  
 20 25 30  
 Val Lys Leu Leu Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr  
 35 40 45  
 Gln Leu Tyr Met Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn  
 50 55 60  
 Ala Leu Glu Leu Ser Gln Leu Glu Asn Arg Ile Leu Asn Gln Thr Ala  
 65 70 75 80  
 Asp Met Leu Gln Leu Ala Ser Lys Tyr Lys Asp Leu Glu His Lys Tyr  
 85 90 95  
 Gln His Leu Ala Thr  
 100

<210> 113  
 <211> 493  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 113

Met	Arg	Pro	Leu	Cys	Val	Thr	Cys	Trp	Trp	Leu	Gly	Leu	Leu	Ala	Ala		
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Met	Gly	Ala	Val	Ala	Gly	Gln	Glu	Asp	Gly	Phe	Glu	Gly	Thr	Glu	Glu		
			20					25					30				
Gly	Ser	Pro	Arg	Glu	Phe	Ile	Tyr	Leu	Asn	Arg	Tyr	Lys	Arg	Ala	Gly		
		35					40					45					
Glu	Ser	Gln	Asp	Lys	Cys	Thr	Tyr	Thr	Phe	Ile	Val	Pro	Gln	Gln	Arg		
	50					55					60						
Val	Thr	Gly	Ala	Ile	Cys	Val	Asn	Ser	Lys	Glu	Pro	Glu	Val	Leu	Leu		
65					70					75					80		
Glu	Asn	Arg	Val	His	Lys	Gln	Glu	Leu	Glu	Leu	Leu	Asn	Asn	Glu	Leu		
				85					90					95			
Leu	Lys	Gln	Lys	Arg	Gln	Ile	Glu	Thr	Leu	Gln	Gln	Leu	Val	Glu	Val		
			100					105						110			
Asp	Gly	Gly	Ile	Val	Ser	Glu	Val	Lys	Leu	Leu	Arg	Lys	Glu	Ser	Arg		
		115					120					125					
Asn	Met	Asn	Ser	Arg	Val	Thr	Gln	Leu	Tyr	Met	Gln	Leu	Leu	His	Glu		
	130					135					140						
Ile	Ile	Arg	Lys	Arg	Asp	Asn	Ala	Leu	Glu	Leu	Ser	Gln	Leu	Glu	Asn		
145					150					155					160		
Arg	Ile	Leu	Asn	Gln	Thr	Ala	Asp	Met	Leu	Gln	Leu	Ala	Ser	Lys	Tyr		
			165						170					175			
Lys	Asp	Leu	Glu	His	Lys	Tyr	Gln	His	Leu	Ala	Thr	Leu	Ala	His	Asn		
			180					185					190				
Gln	Ser	Glu	Ile	Ile	Ala	Gln	Leu	Glu	Glu	His	Cys	Gln	Arg	Val	Pro		
		195					200					205					
Ser	Ala	Arg	Pro	Val	Pro	Gln	Pro	Pro	Pro	Ala	Ala	Pro	Pro	Arg	Val		
	210					215					220						
Tyr	Gln	Pro	Pro	Thr	Tyr	Asn	Arg	Ile	Ile	Asn	Gln	Ile	Ser	Thr	Asn		
225					230					235					240		
Glu	Ile	Gln	Ser	Asp	Gln	Asn	Leu	Lys	Val	Leu	Pro	Pro	Pro	Leu	Pro		
				245					250					255			
Thr	Met	Pro	Thr	Leu	Thr	Ser	Leu	Pro	Ser	Ser	Thr	Asp	Lys	Pro	Ser		
			260					265					270				
Gly	Pro	Trp	Arg	Asp	Cys	Leu	Gln	Ala	Leu	Glu	Asp	Gly	His	Asp	Thr		
		275					280					285					
Ser	Ser	Ile	Tyr	Leu	Val	Lys	Pro	Glu	Asn	Thr	Asn	Arg	Leu	Met	Gln		
						295					300						

Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr Val Ile Gln  
305 310 315 320

Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp Glu Thr Tyr  
325 330 335

Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu Gly Leu Glu  
340 345 350

Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu Leu Val Thr  
355 360 365

Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr Ala Ser Phe  
370 375 380

Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr  
385 390 395 400

His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe  
405 410 415

Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His  
420 425 430

Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu  
435 440 445

Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp  
450 455 460

Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser Leu Lys Lys  
465 470 475 480

Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His  
485 490

<210> 114

<211> 54

<212> PRT

<213> Homo sapiens

<400> 114

Thr Asn Lys Leu Glu Arg Gln Met Leu Met Gln Ser Arg Glu Leu Gln  
1 5 10 15

Arg Leu Gln Gly Arg Asn Arg Ala Leu Glu Thr Arg Leu Gln Ala Leu  
20 25 30

Glu Ala Gln His Gln Ala Gln Leu Asn Ser Leu Gln Glu Lys Arg Glu  
35 40 45

Gln Leu His Ser Leu Leu  
50

<210> 115

<211> 145

<212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 115

Thr Gln Gln Val Lys Gln Leu Glu Gln Ala Leu Gln Asn Asn Thr Gln  
 1 5 10 15  
 Trp Leu Lys Lys Leu Glu Arg Ala Ile Lys Thr Ile Leu Arg Ser Lys  
 20 25 30  
 Leu Glu Gln Val Gln Gln Gln Met Ala Gln Asn Gln Thr Ala Pro Met  
 35 40 45  
 Leu Glu Leu Gly Thr Ser Leu Leu Asn Gln Thr Thr Ala Gln Ile Arg  
 50 55 60  
 Lys Leu Thr Asp Met Glu Ala Gln Leu Leu Asn Gln Thr Ser Arg Met  
 65 70 75 80  
 Asp Ala Gln Met Pro Glu Thr Phe Leu Ser Thr Asn Lys Leu Glu Asn  
 85 90 95  
 Gln Leu Leu Leu Gln Arg Gln Lys Leu Gln Gln Leu Gln Gly Gln Asn  
 100 105 110  
 Ser Ala Leu Glu Lys Arg Leu Gln Ala Leu Glu Thr Lys Gln Gln Glu  
 115 120 125  
 Glu Leu Ala Ser Ile Leu Ser Lys Lys Ala Lys Leu Leu Asn Thr Leu  
 130 135 140

Ser  
 145

&lt;210&gt; 116

&lt;211&gt; 465

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 116

gcccatggag agactgctg caggccctgg aggatggcca cgacaccagc tccatctacc 60  
 tggatgaagcc ggagaacacc aaccgcctca tgcagggtgtg gtgcgaccag agacacgacc 120  
 ccgggggctg gaccgtcatc cagagacgcc tggatggctc tgttaacttc ttcaggaact 180  
 gggagacgta caagcaagggt tttgggaaca ttgacggcga atactggctg ggcctggaga 240  
 acatttactg gctgacgaac caaggcaact acaaactcct ggtgaccatg gaggactggt 300  
 ccggccgcaa agtctttgca gaatacgcca gtttccgcct ggaacctgag agcgagtatt 360  
 ataagctgcg gctggggcgc taccatggca atgcgggtga ctctttaca tggcacaacg 420  
 gcaagcagtt caccacccag gacagagatc atgatgtcta cacag 465

&lt;210&gt; 117

&lt;211&gt; 305

&lt;212&gt; DNA

<213> Homo sapiens

<400> 117

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ggattgccag gagctgttcc aggttgggga gaggcagagt ggactatttg aaatccagcc      60
tcaggggtct ccgccatttt tggatgaactg caagatgacc tcagatggag gctggacagt      120
aattcagagg cgccacgatg gctcagtgga cttcaaccgg ccctkggtag cctacaaggc      180
ggtgggttttg ggggatcccc acggcgagtt ctggcttggg tcttggagaa aggkgcatag      240
catcacgggg ggaccggaac agccgmctgg ccgtgcaamc tgcgggggact gggatgggca      300
aacgc                                             305

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<210> 118

<211> 458

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (224)..(244)

<223> "n" may be any nucleotide

<220>

<221> misc\_feature

<222> (347)..(347)

<223> "n" may be any nucleotide

<220>

<221> misc\_feature

<222> (353)..(353)

<223> "n" may be any nucleotide

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<221> misc\_feature

<222> (384)..(384)

<223> "n" may be any nucleotide

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<221> misc\_feature

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<223> "n" may be any nucleotide

<400> 118

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acggcaagca gttcaccacc ctggacagag atcatgatgt ctacacagga aactgtgccc      120
actaccagaa gggaggctgg tggatataacg cctgtgcccc ctccaacctc aaccgggggtc      180
tggataccgc gggggcatta ccggagccgc taccaggacg gagngtactg ggctgagttc      240

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cgaggaggct cttactcact caaggaaaacg tggatgatgat gatccgaccg aaccccaaca 300  
 ccttccacta agccagctcc ccctcctgac ctctccgtgg ccattgncag gangcccacc 360  
 ctggtcacgc tggccacagc acanagaaca actcctcacn agttcatcct gaggctggga 420  
 ggaccgggat gctggattct gttttnccga agtcactg 458

<210> 119  
 <211> 173  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 119  
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 ggcaagcagt tcaccaccct ggacagagat catgatgtct acacaggaaa ctgtgcccac 120  
 taccagaagg gaggctggtg gtataacgcc tgtgcccact ccaacctcaa ccg 173

<210> 120  
 <211> 638  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 120  
 gcccattggag agactgcctg caggccctgg aggatggcca cgacaccagc tccatctacc 60  
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 ccgggggctg gaccgtcatc cagagacgcc tggatggctc tgttaacttc ttcaggaact 180  
 gggagacgta caagcaaggg tttgggaaca ttgacggcga atactggctg ggccctggaga 240  
 acatttactg gctgacgaac caaggcaact acaaactcct ggtgaccatg gaggactggt 300  
 ccggccgcaa agtctttgca gaatacgcca gtttccgcct ggaacctgag agcgagtatt 360  
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 gcaagcagtt caccacccag gacagagatc atgatgtcta cacagtataa gctgcggtg 480  
 gggcgatacc atggcaatgc gggtgactcc tttacatggc acaacggcaa gcagttcacc 540  
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<210> 121



<211> 4045  
 <212> DNA  
 <213> Artificial sequence

<220>  
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<400> 121  
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 ccgggggctg gaccgtcatc cagagacgcc tggatggctc tgttaacttc ttcaggaact 180  
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 ccggccgcaa agtcctttgca gaatacgcca gtttccgcct ggaacctgag agcgagtatt 360  
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 gcaagcagtt caccacccag gacagagatc atgatgtcta cacagtataa gctgcggctg 480  
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 tgggtggtata acgcctgtgc ccactccaac ctcaaccgga aaaagagagg aagagaaacc 660  
 atttagagac tgtgcagatg tatatcaagc tggttttaat aaaagtggaa tctacactat 720  
 ttatattaat aatatgccag aacccaaaaa ggtgttttgc aatatggatg tcaatggggg 780  
 aggttggact gtaatacaac atcgtgaaga tggaagtcta gatttccaaa gaggctggaa 840  
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ttgggggtgac agtgctcacg tggctcgact atagaaaact ccactgactg tcggggcttta	1560
aaaaggggaag aaactgctga gcttgctgtg cttcaaacta ctactggacc ttatttttga	1620
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attttgataa aaatttagaa cagcattgtc ctctgagttg gttaaatggt aatggatttc	1860
agaagcctaa ttccagtatc atacttacta gttgatttct gcttaccat cttcaaatga	1920
aaattccatt tttgtaagcc ataatagaact gtagtacatg gacaataagt gtgtggtaga	1980
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agtaaggatg tatgtgggta aaacttacca ccccatact atggttttca tttactctaa	2100
aaactgattg aatgatatat aaatatattt atagcctgag taaagttaaa agaattgtaa	2160
atatatcatc aagttcttaa aataatatac atgcatttaa tatttccttt gatattatac	2220
aggaaagcaa tattttggag tatgttaagt tgaagtaaaa ccaagtactc tggagcagtt	2280
cattttacag tatctacttg catgtgtata catacatgta acttcattat tttaaaaata	2340
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tgaacatgc ttaccagatt cacactgttc cagtgtctat aaaagaaaca ctttgaagtc	2460
tataaaaaat aaaataatta taaatatcat tgtacatagc atgtttatat ctgcaaaaaa	2520
cctaatagct aattaatctg gaatatgcaa cattgtcctt aattgatgca aataacacaa	2580
atgctcaaag aaatctacta tatcccttaa tgaatacat cattcttcat atatttctcc	2640
ttcagtccat tcccttaggc aatttttaat ttttaaaaat tattatcagg ggagaaaaat	2700
tggcaaaact attatatgta agggatatat atatacaaaa agaaaattaa tcatagtcac	2760
ctgactaaga aattctgact gctagttgcc ataaataact caatggaaat attcctatgg	2820
gataatgtat ttttaagtga tttttggggt gcttgaagtt actgcattat tttatcaaga	2880
agtcttctct gcctgtaagt gtccaagggt atgacagtaa acagttttta ttaaaacatg	2940
agtcactatg ggatgagaaa attgaaataa agctactggg cctcctctca taaaagagac	3000
agttgttggc aaggtagcaa taccagtttc aaacttgggtg acttgatcca ctatgcctta	3060
atggtttctt ccatttgaga aaataaagct attcacattg ttaagaaaaa tactttttta	3120
agtttaccat caagtctttt ttatatattt gtgtctgtat tctaccctt tttgccttac	3180
aagtgatatt tgcagggtatt ataccatttt tctattcttg gtggcttctt catagcaggt	3240

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aagcctctcc ttctaaaaac ttctcaactg ttttcattta agggaaagaa aatgagtatt 3300
ttgtcctttt gtgttcctac agacactttc ttaaaccagt ttttggataa agaatactat 3360
ttccaaactc atattacaaa aacaaaataa aataataaaa aaagaaagca tgatatttac 3420
tgttttgttg tctgggtttg agaaatgaaa tattgtttcc aattatttat aataaatcag 3480
tataaaatgt tttatgattg ttatgtgtat tatgtaatac gtacatgttt atggcaattt 3540
aacatgtgta ttcttttcat ttaattgttt cagaatagga taattaggta ttcgaatttt 3600
gtcttttaaaa ttcatgtggg ttctatgcaa agttcttcat atcatcacia cattatttga 3660
tttaataaaa attgaaagtg cacccatggc agaaggagga gggcagaatc atcacgaagt 3720
gggtgaagttc atggatgtct atcagcgcag ctactgccat ccaatcgaga ccctgggtgga 3780
catcttccag gagtaccctg atgagatcga gtacatcttc aagccatcct gtgtgcccct 3840
gatgcgatgc gggggctgct gcaatgacga gggcctggag tgtgtgcca ctgaggagtc 3900
caacatcacc atgcagatta tgcggatcaa acctaccaa ggccagcaca taggagagat 3960
gagcttcccta cagcacaaca aatgtgaatg cagaccaaag aaagatagag caagacaaga 4020
aaaatgtgac aagccgaggc ggtga 4045

```

```

<210> 122
<211> 280
<212> PRT
<213> Artificial sequence

```

```

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

```

```

<400> 122

```

```

Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala
1          5          10          15
Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys
20          25          30
Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
35          40          45
Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
50          55          60
Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
65          70          75          80
Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys
85          90          95
Val Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile

```

100	105	110
Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly		
115	120	125
Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp		
130	135	140
Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu		
145	150	155
Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp		
165	170	175
Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu		
180	185	190
Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser		
195	200	205
Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn		
210	215	220
Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile Val Thr Ala Thr Val Asn		
225	230	235
Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn		
245	250	255
Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ala Ala Lys Asp Pro Thr		
260	265	270
Val Ala Lys Glu Glu Gln Ile Ser		
275	280	

<210> 123  
 <211> 221  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 123

Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly
1 5 10 15
Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu
20 25 30
Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr
35 40 45
Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp
50 55 60
Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu
65 70 75 80
Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu
85 90 95

Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr  
                   100                  105                  110  
 Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu  
                   115                  120                  125  
 Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His  
                   130                  135                  140  
 Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys  
                   145                  150                  155                  160  
 Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly  
                   165                  170                  175  
 Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln Asn His Gly  
                   180                  185                  190  
 Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser  
                   195                  200                  205  
 Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe  
                   210                  215                  220

<210> 124  
 <211> 1506  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 124  
 atgtggcaga ttgttttctt tactctgagc tgtgatcttg tcttggccgc agcctataac 60  
 aactttcgga agagcatgga cagcatagga aagaagcaat atcaggtcca gcatgggtcc 120  
 tgcagctaca ctttctctct gccagagatg gacaactgcc gctcttcttc cagcccctac 180  
 gtgtccaatg ctgtgcagag ggacgcgccg ctccaatacg atgactcggt gcagaggctg 240  
 caagtgtctg agaacatcat ggaaaacaac actcagtggc taatgaagggt agagaatata 300  
 tcccaggaca acatgaagaa agaaatggta gagatacagc agaatgcagt acagaaccag 360  
 acggctgtga tgatagaaat agggacaaac ctgttgaacc aaacagcgga gcaaacgcgg 420  
 aagttaactg atgtggaagc ccaagtatta aatcagacca cgagacttga acttcagctc 480  
 ttggaacact ccctctcgac aaacaaattg gaaaaacaga ttttggacca gaccagtga 540  
 ataaacaaat tgcaagataa gaacagtttc ctagaaaaga aggtgctagc tatggaagac 600  
 aagcacatca tccaactaca gtcaataaaa gaagagaaag atcagctaca ggtgttagta 660  
 tccaagcaga attccatcat tgaagaactc gaaaaaaaaa tagtgactgc cacggtgaat 720

```

aattcagttc ttcagaagca gcaacatgat ctcatggaga cagttaataa cttactgact 780
atgatgtcca catcaaacgc agctaaggac cccactgttg ctaaagaaga acaaatcagc 840
gaggaagaga aaccatttag agactgtgca gatgtatatc aagctgggtt taataaaagt 900
ggaatctaca ctatttatat taataatatg ccagaaccca aaaaggtggt ttgcaatatg 960
gatgtcaatg ggggagggtg gactgtaata caacatcgtg aagatggaag tctagatttc 1020
caaagaggct ggaaggaata taaaatgggt tttggaaatc cctccggtga atattggctg 1080
gggaatgagt ttatTTTTGC cattaccagt cagaggcagt acatgctaag aattgagtta 1140
atggactggg aagggaaaccg agcctattca cagtatgaca gattccacat aggaaatgaa 1200
aagcaaaaact ataggttgta tttaaaaggt cacactggga cagcaggaaa acagagcagc 1260
ctgatcttac acggtgctga tttcagcact aaagatgctg ataatgacaa ctgtatgtgc 1320
aaatgtgccc tcatgttaac aggaggatgg tggtttgatg cttgtggccc ctccaatcta 1380
aatggaatgt tctatactgc gggacaaaac catggaaaac tgaatgggat aaagtggcac 1440
tacttcaaag ggcccagtta ctccttacgt tccacaacta tgatgattcg acctttagat 1500
ttttga 1506

```

```

<210> 125
<211> 501
<212> PRT
<213> Artificial sequence

```

```

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

```

```

<400> 125

```

```

Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala
1          5          10          15
Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys
20          25          30
Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
35          40          45
Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
50          55          60
Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
65          70          75          80
Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys
85          90          95

```

Val Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile  
 100 105 110  
 Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly  
 115 120 125  
 Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp  
 130 135 140  
 Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu  
 145 150 155 160  
 Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp  
 165 170 175  
 Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu  
 180 185 190  
 Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser  
 195 200 205  
 Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn  
 210 215 220  
 Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile Val Thr Ala Thr Val Asn  
 225 230 235 240  
 Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn  
 245 250 255  
 Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ala Ala Lys Asp Pro Thr  
 260 265 270  
 Val Ala Lys Glu Glu Gln Ile Ser Glu Glu Glu Lys Pro Phe Arg Asp  
 275 280 285  
 Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr  
 290 295 300  
 Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met  
 305 310 315 320  
 Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly  
 325 330 335  
 Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly  
 340 345 350  
 Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile  
 355 360 365  
 Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu  
 370 375 380  
 Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu  
 385 390 395 400  
 Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly  
 405 410 415

Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp  
                     420                    425                    430  
 Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly  
                     435                    440                    445  
 Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe  
                     450                    455                    460  
 Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His  
                     465                    470                    475                    480  
 Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile  
                     485                    490                    495  
 Arg Pro Leu Asp Phe  
                     500

<210> 126  
 <211> 648  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <221> misc\_feature  
 <222> ()..()  
 <223> Synthetic

<400> 126

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
 1                    5                    10                    15  
 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
                     20                    25                    30  
 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
                     35                    40                    45  
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
                     50                    55                    60  
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
                     65                    70                    75                    80  
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
                     85                    90                    95  
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
                     100                    105                    110  
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
                     115                    120                    125  
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys  
                     130                    135                    140  
 Pro Arg Arg Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu



145		150		155		160									
Val	Leu	Ala	Ala	Ala	Tyr	Asn	Asn	Phe	Arg	Lys	Ser	Met	Asp	Ser	Ile
			165						170					175	
Gly	Lys	Lys	Gln	Tyr	Gln	Val	Gln	His	Gly	Ser	Cys	Ser	Tyr	Thr	Phe
			180					185					190		
Leu	Leu	Pro	Glu	Met	Asp	Asn	Cys	Arg	Ser	Ser	Ser	Ser	Pro	Tyr	Val
		195					200					205			
Ser	Asn	Ala	Val	Gln	Arg	Asp	Ala	Pro	Leu	Glu	Tyr	Asp	Asp	Ser	Val
	210					215					220				
Gln	Arg	Leu	Gln	Val	Leu	Glu	Asn	Ile	Met	Glu	Asn	Asn	Thr	Gln	Trp
225					230					235					240
Leu	Met	Lys	Val	Glu	Asn	Ile	Ser	Gln	Asp	Asn	Met	Lys	Lys	Glu	Met
				245					250					255	
Val	Glu	Ile	Gln	Gln	Asn	Ala	Val	Gln	Asn	Gln	Thr	Ala	Val	Met	Ile
			260					265					270		
Glu	Ile	Gly	Thr	Asn	Leu	Leu	Asn	Gln	Thr	Ala	Glu	Gln	Thr	Arg	Lys
		275					280					285			
Leu	Thr	Asp	Val	Glu	Ala	Gln	Val	Leu	Asn	Gln	Thr	Thr	Arg	Leu	Glu
	290					295					300				
Leu	Gln	Leu	Leu	Glu	His	Ser	Leu	Ser	Thr	Asn	Lys	Leu	Glu	Lys	Gln
305					310					315					320
Ile	Leu	Asp	Gln	Thr	Ser	Glu	Ile	Asn	Lys	Leu	Gln	Asp	Lys	Asn	Ser
			325					330					335		
Phe	Leu	Glu	Lys	Lys	Val	Leu	Ala	Met	Glu	Asp	Lys	His	Ile	Ile	Gln
			340					345					350		
Leu	Gln	Ser	Ile	Lys	Glu	Glu	Lys	Asp	Gln	Leu	Gln	Val	Leu	Val	Ser
		355					360					365			
Lys	Gln	Asn	Ser	Ile	Ile	Glu	Glu	Leu	Glu	Lys	Lys	Ile	Val	Thr	Ala
	370					375					380				
Thr	Val	Asn	Asn	Ser	Val	Leu	Gln	Lys	Gln	Gln	His	Asp	Leu	Met	Glu
385					390					395					400
Thr	Val	Asn	Asn	Leu	Leu	Thr	Met	Met	Ser	Thr	Ser	Asn	Ala	Ala	Lys
				405					410					415	
Asp	Pro	Thr	Val	Ala	Lys	Glu	Glu	Gln	Ile	Ser	Glu	Glu	Glu	Lys	Pro
			420					425					430		
Phe	Arg	Asp	Cys	Ala	Asp	Val	Tyr	Gln	Ala	Gly	Phe	Asn	Lys	Ser	Gly
		435					440					445			
Ile	Tyr	Thr	Ile	Tyr	Ile	Asn	Asn	Met	Pro	Glu	Pro	Lys	Lys	Val	Phe
	450					455					460				

Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg  
 465 470 475 480  
 Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met  
 485 490 495  
 Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile  
 500 505 510  
 Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met  
 515 520 525  
 Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile  
 530 535 540  
 Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly  
 545 550 555 560  
 Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser  
 565 570 575  
 Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met  
 580 585 590  
 Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn  
 595 600 605  
 Gly Met Phe Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile  
 610 615 620  
 Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr  
 625 630 635 640  
 Met Met Ile Arg Pro Leu Asp Phe  
 645